Exhibit C

Blast of SEQ ID NO: 1 versus human genome

MEGABLAST 1.2.3-Paracel [2001-11-20]

Reference:
Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000),
"A greedy algorithm for aligning DNA sequences",
J Comput Biol 2000; 7(1-2):203-14.
Database: Homo_sapiens.latestgp.masked.fa
          33,840 sequences; 200,810,911,373 total letters

Query= LEX121seqid1
        (747 letters)

Sequences producing significant alignments:	Score (bits)	E Value
AC135034.1.27032.29361	287	5e-75
AC025418.23.1.83000	287	5e-75
AC135034.1.59399.65233	174	5e-41

>AC135034.1.27032.29361
          Length = 2330

 Score = 287 bits (145), Expect = 5e-75
 Identities = 145/145 (100%)
 Strand = Plus / Plus

```
Query: 451   ttacagtgttgtggccaacataattacacagactggataaagaataagaacaaagaaaat 510
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1180  ttacagtgttgtggccaacataattacacagactggataaagaataagaacaaagaaaat 1239


Query: 511   tcaggacaggtgccatgttcttgcacaaagtcaactttaagaaaatggttttgtgatgag 570
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1240  tcaggacaggtgccatgttcttgcacaaagtcaactttaagaaaatggttttgtgatgag 1299


Query: 571   ccactgaatgcaacttaccttgagg 595
             |||||||||||||||||||||||||
Sbjct: 1300  ccactgaatgcaacttaccttgagg 1324
```

>AC025418.23.1.83000
          Length = 83000

 Score = 287 bits (145), Expect = 5e-75
 Identities = 145/145 (100%)
 Strand = Plus / Minus

```
Query: 451    ttacagtgttgtggccaacataattacacagactggataaagaataagaacaaagaaaat 510
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 48068  ttacagtgttgtggccaacataattacacagactggataaagaataagaacaaagaaaat 48009
```

```
Query: 511    tcaggacaggtgccatgttcttgcacaaagtcaactttaagaaaatggttttgtgatgag 570
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 48008  tcaggacaggtgccatgttcttgcacaaagtcaactttaagaaaatggttttgtgatgag 47949


Query: 571    ccactgaatgcaacttaccttgagg 595
               |||||||||||||||||||||||||
Sbjct: 47948  ccactgaatgcaacttaccttgagg 47924



 Score =  250 bits (126), Expect = 1e-63
 Identities = 126/126 (100%)
 Strand = Plus / Minus


Query: 139    gatgaaaataatcacttcatagtacctatttctcaaattttgattggaatgggatcttct 198
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 58492  gatgaaaataatcacttcatagtacctatttctcaaattttgattggaatgggatcttct 58433


Query: 199    actgttcttttttgtctattgggttatataggaattcacaacgaaatcagatggctccta 258
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 58432  actgttcttttttgtctattgggttatataggaattcacaacgaaatcagatggctccta 58373


Query: 259    attgtg 264
               ||||||
Sbjct: 58372  attgtg 58367



 Score =  224 bits (113), Expect = 6e-56
 Identities = 113/113 (100%)
 Strand = Plus / Minus


Query: 338    aggttcagcaactatggcatgacaaaattgattttgtcatttctgagtatggatctaaag 397
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 50207  aggttcagcaactatggcatgacaaaattgattttgtcatttctgagtatggatctaaag 50148


Query: 398    ataagcctgaagatataaccaagtggactattctgaatgccttacagaaaaca 450
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 50147  ataagcctgaagatataaccaagtggactattctgaatgccttacagaaaaca 50095



 Score =  174 bits (88), Expect = 5e-41
 Identities = 88/88 (100%)
 Strand = Plus / Minus


Query: 593    agggttgtgaaaataaaatcagtgcatggtataatgttaatgtgttaaccttaatcggaa 652
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 46442  agggttgtgaaaataaaatcagtgcatggtataatgttaatgtgttaaccttaatcggaa 46383


Query: 653    ttaactttggacttttaacttcagaggt 680
               ||||||||||||||||||||||||||||
```

```
Sbjct: 46382  ttaactttggactttaacttcagaggt  46355


   Score =  155 bits (78), Expect = 5e-35
   Identities = 78/78 (100%)
   Strand = Plus / Minus


 Query: 264    gtatgcagtattgataacatggacctttgctgttcaggttgtactttcagcattcatcat  323
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 53869  gtatgcagtattgataacatggacctttgctgttcaggttgtactttcagcattcatcat  53810


 Query: 324    cacaaagaaagaggaggt  341
               ||||||||||||||||||
 Sbjct: 53809  cacaaagaaagaggaggt  53792



   Score =  147 bits (74), Expect = 1e-32
   Identities = 74/74 (100%)
   Strand = Plus / Minus


 Query: 66     ggttcttggactttattcatgggatttggtgcatggctcttattagatagaaataattt  125
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 60260  ggttcttggactttattcatgggatttggtgcatggctcttattagatagaaataattt  60201


 Query: 126    tttaacagcttttg  139
               ||||||||||||||
 Sbjct: 60200  tttaacagcttttg  60187



   Score =  141 bits (71), Expect = 7e-31
   Identities = 71/71 (100%)
   Strand = Plus / Minus


 Query: 677    aggttttccaagtctcattaacagtttgtttcttcaaaaacatcaagaatataatccatg  736
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 45026  aggttttccaagtctcattaacagtttgtttcttcaaaaacatcaagaatataatccatg  44967


 Query: 737    cagaaatgtga  747
               |||||||||||
 Sbjct: 44966  cagaaatgtga  44956



   Score =  135 bits (68), Expect = 4e-29
   Identities = 68/68 (100%)
   Strand = Plus / Minus


 Query: 1      atgttaagaaataacaaaacaataattattaagtactttcttaatctcattaatggagct  60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 60414  atgttaagaaataacaaaacaataattattaagtactttcttaatctcattaatggagct  60355
```

```
Query: 61      ttcttggt 68
               | |||||||
Sbjct: 60354 ttcttggt 60347



>AC135034.1.59399.65233
         Length = 5835

 Score =  174 bits (88), Expect = 5e-41
 Identities = 88/88 (100%)
 Strand = Plus / Minus


Query: 593   agggttgtgaaaataaaatcagtgcatggtataatgttaatgtgttaaccttaatcggaa 652
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 5352  agggttgtgaaaataaaatcagtgcatggtataatgttaatgtgttaaccttaatcggaa 5293


Query: 653   ttaactttggacttttaacttcagaggt 680
             ||||||||||||||||||||||||||||
Sbjct: 5292  ttaactttggacttttaacttcagaggt 5265



 Score =  141 bits (71), Expect = 7e-31
 Identities = 71/71 (100%)
 Strand = Plus / Minus


Query: 677   aggttttccaagtctcattaacagtttgtttcttcaaaaacatcaagaatataatccatg 736
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3942  aggttttccaagtctcattaacagtttgtttcttcaaaaacatcaagaatataatccatg 3883


Query: 737   cagaaatgtga 747
             |||||||||||
Sbjct: 3882  cagaaatgtga 3872
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